Genome Sequence of *Phytophthora ramorum*: Implications for Management[1]

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Abstract

A draft genome sequence has been determined for *Phytophthora ramorum*, together with a draft sequence of the soybean pathogen *Phytophthora sojae*. The *P. ramorum* genome was sequenced to a depth of 7-fold coverage, while the *P. sojae* genome was sequenced to a depth of 9-fold coverage. The genome size of *P. ramorum* was estimated to be significantly smaller than that of *P. sojae*, 65 Mb compared to 95 Mb, with the difference lying primarily in the amount of repetitive sequences in the *P. sojae* genome. Computer predictions estimate the number of genes in *P. ramorum* to be 15,743, while 19,027 are predicted for *P. sojae*. Most of the differences in gene number result from larger multigene families in *P. sojae*. Six hundred twenty four genes were predicted to be unique to *P. ramorum*, while 1755 were predicted to be unique to *P. sojae*. The generally high level of similarity of most *P. ramorum* and *P. sojae* genes predicts that, in general, chemical treatments developed for other *Phytophthora* species should also be effective against *P. ramorum*. The small size of the *P. ramorum* genome and lack of extensive numbers of duplicated chromosomal segments effectively eliminates the hypothesis that *P. ramorum* is a recent hybrid between two other *Phytophthora* species. The two *Phytophthora* genome sequences are available at http://genome.jgi-psf.org/ and http://phytophthora.vbi.vt.edu.

A critical need in understanding the epidemiology of *P. ramorum* is the need to be able to distinguish different genetic individuals of *P. ramorum* so that patterns of spread can be traced. However, very little genetic variation can be detected in *P. ramorum* isolates from the United States, using conventional techniques such as AFLPs (Ivors and others 2004), presumably because most of the population has derived clonally from a single introduction or a small number of introductions of closely related strains. The *P. ramorum* genome sequence now offers the possibility of examining the genome directly for regions that may be useful in genetically distinguishing closely related strains. Simple Sequence Repeats (SSRs) or microsatellites have been used for genetic typing of an extensive variety of eukaryotic organisms. A total of 1,000 microsatellite loci were observed in the genome of *P. ramorum*.

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Dinucleotide repeats were the most abundant microsatellite repeats making up 56 percent of all repeats followed by trinucleotide repeats at 29 percent. Single Nucleotide Polymorphisms (SNPs) offer another resource for identifying recent variation, such as gene conversion or mitotic crossing over (Chamnanpunt and others 2001). Sequencing of the *P. ramorum* genome identified approximately 200,000 sites at which the genome sequence of this diploid organism is polymorphic. Screening of these SSR and SNP sites is underway to determine whether any of these sites are variable enough to detect recent genetic divergence in the *P. ramorum* population that could be used to track patterns of spread.

References

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